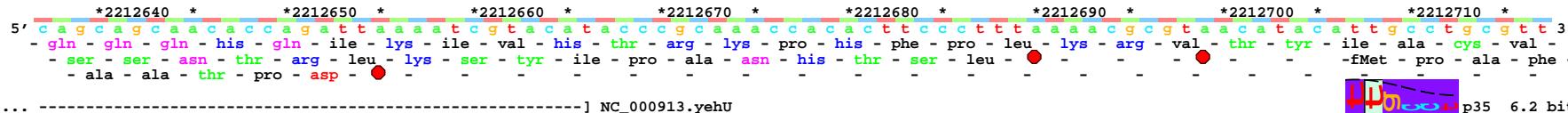
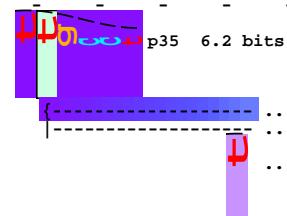


- 1 -

piece 1, NC_000913, yehU_mlrA+, config: linear, direction: +, begin: 2212637, end: 2212907



---1 NC 000913.yehU



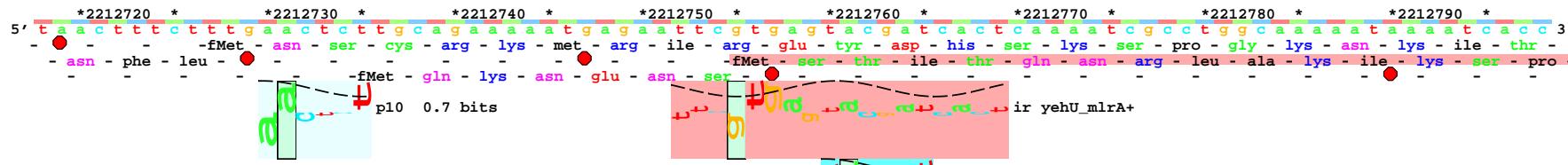
... p3
... p3

... p35-(23)-p10 2212731 Gap

... p35-p10 2212731 total 5.5

-35-

... p35



... ----- } p35-(23)-p10 2212731 Gap 1.4 bits

5.0 bits

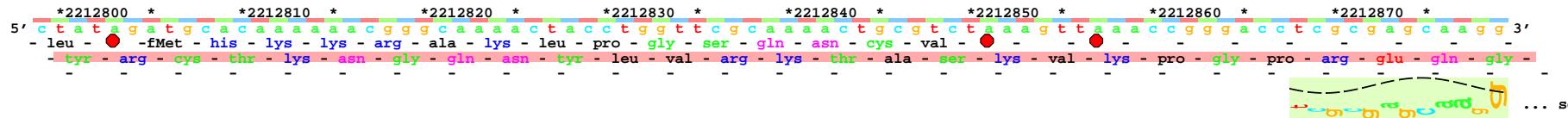
Phylogenetic tree diagram showing node types and bit values:

- p35 2.8 bits
- sd 2.4 bits
- sd-ir 8.1 bits
- p10 3.8 bits

```
{-----} p35-(24)-p10 2212742 Gap 2.4 bits  
{-----} p35-p10 2212742 total 4.2 bits
```

p35 5.2 bits

```
{-----} p35-(25)-p10 2212761 Gap 4.0 bits  
|-----| p35-p10 2212761 total 6.2 bits
```



The diagram illustrates the genomic context of the **orf 43 codons** (green box) and the **ir yehU_mlrA+** intergenic region (pink box). The **orf 43 codons** are preceded by a promoter region (blue box) and followed by a transcription start site (red arrow). The **ir yehU_mlrA+** intergenic region contains a transcription start site (red arrow) and a poly-A tail (green bar).

```
{-----} sd-(8)-ir 2212888 Gap 2.4 bits  
|-----| sd-ir 2212888 yehU_mlrA+ total 6.3 bits
```